

T-DNA 3' SENSE SEQUENCE

5'	C	CGC	TGC	AGC	CGC	CGC	TTT	CTG	CGG	CCT	GGG	CCT	CTC	GCC	GTC	AGC	ATG	CCA	CAC
		9		18		27											45		54
																	M	P	H
		63		72		81											99		108
A	F	K	P	G	D	L	V	F	A	K	M	K	G	Y	P	H	W		
		117		126		135											153		162
P	A	R	I	D	D	I	A	D	G	A	V	K	P	P	P	N	K		
		171		180		189											207		216
TAC	CCC	ATC	TTT	TTC	TTT	GGC	ACA	CAC	GAA	ACA	GCA	TTC	CTG	GGC	CCC	AAA	GAC		
Y	P	I	F	F	F	G	T	H	E	T	A	F	L	G	P	K	D		
		225		234		243											261		270
CTC	TTC	CCT	TAC	GAG	GAA	TCC	AAG	GAG	AAG	TTT	GGC	AAG	CCC	AAC	AAG	AGG	AAA		
L	F	P	Y	E	E	S	K	E	K	F	G	K	P	N	K	R	K		
		279		288		297											315		324
GGG	TTC	AGC	GAG	GGG	CTG	TGG	GAG	ATC	GAG	AAC	AAC	CCT	ACT	GTC	AAG	GCT	TCC		
G	F	S	E	G	L	W	E	I	E	N	N	P	T	V	K	A	S		
		333		342		351											369		378
GGC	TAT	CAG	TCC	TCC	CAG	AAA	AAG	AGC	TGT	GTA	GAG	CCT	GAA	CCA	GAG	CCC			
G	Y	Q	S	S	Q	K	K	S	C	V	E	E	P	E	P	E	P		

FIGURE 1A

GAA	GCT	GCA	GAG	GGT	GAC	GGT	GAT	AAG	AAG	GGG	AAT	GCA	GAG	GGC	AGC	AGC	GAC
E	A	A	E	G	D	G	D	K	K	N	A	E	G	S	S	D	
GAG	GAA	GGG	AAG	CTG	GTC	ATT	GAT	GAG	CCA	GCC	AAG	GAG	AAG	AAA	GGA		
E	E	G	K	L	V	I	D	E	P	A	K	E	K	N	E	K	G
GCG	TTG	AAG	AGG	AGA	GCA	GGG	GAC	TTG	CTG	GAG	GAC	TCT	CCT	AAA	CGT	CCC	AAG
A	L	K	R	R	A	G	D	L	L	E	D	S	P	K	R	P	K
549		558		504		513		567		522		531		585		540	
GAG	GCA	GAA	AAC	CCT	GAA	GGG	GAG	GAG	AAG	GAG	GCA	GCC	ACC	TTC	GAG	GTT	GAG
E	A	E	N	P	E	G	E	E	K	E	A	A	T	L	E	V	E
603		612		621		630		675		576		585		594			
AGG	CCC	CTT	CCT	ATG	GAG	GTG	GAA	AAG	AAT	AGC	ACC	CCC	TCT	GAG	CCC	GGC	TCT
R	P	L	P	M	E	V	E	K	N	S	T	P	S	E	P	G	S
657		666		675		684		684		630		639		648			
GGC	CGG	GGG	CCT	CCC	CNN	NNN	NAG	GAA	GAG	GCT							
G	R	G	P	P	X	X	X	X	X	X	X	X	X	X	E	E	A
711		720		729		738		729		738		747		756			
ACC	AAG	GAA	GAT	GCT	GAG	GCC	CCA	GGC	ATC	AAG	AGT	CAT	GAG	AGC	CTG	TAG	CCA
T	K	E	D	A	E	A	P	G	I	K	S	H	E	S	L		

FIGURE 1B

T U H E S O " S E S S E N D

CCA ATG TTT CAA GAG GAG CCC CCA CCC TGT TCC TGC TGC TGC TGT CTG GGT GCT ACT
765 774 783 792 801 810
GGG GAA ACT GGC CAT GGG CTG CAA ACT GGG NAC CCC TTT TCC ANC ANC NCA ANC TGN
819 828 837 846 855 864

TNT TCT T 3'

FIGURE 1C

1 MP HA - - - F K P G D L V F A K M K G Y P H W P A R I D D I A D G A V K P 876242
 1 M S R S N R Q R E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 598956
 1 M S R S N R Q R E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 945419
 36 P N K Y P I F F F G T H E T A F L G P K D L F P Y E E S K E R F G K P N K R K 876242
 4L T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E R F G K P N K R K GI 598956
 4L T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E R F G K P N K R K GI 945419
 76 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E A E 876242
 8L G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E A E GI 598956
 8L G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E A E GI 945419
 116 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D 876242
 121 G D G D K K G S A E G S S D E E G K L V I D E P A K E K N E K G T L K R R A G D GI 598956
 121 G D G D K K G S A E G S S D E E G K L V I D E P A K E K N E K G T L K R R A G D GI 945419
 156 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T 876242
 161 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T GI 598956
 161 [V] L L E D S P K R P K E E D K E I A A L E G E R H L P V E V E K N S T GI 945419
 196 P S E P G S G R G P P X X X X X X X X E E A T K E D A E A P G I K S H E S L 876242
 201 P S E P G S G R G P P Q E E E E E D E E E A T K E D A E A P G I R D H E S L GI 598956
 201 P S E P D S G Q G P P A E E E E E E E E E A A A K E E A A P G V R D H E S L GI 945419

FIGURE 2

TUNING SPACES

1 CCGCTGCAAGCCGCTTCTGGCCTGGCTTGCGCTCTCGCCCTCGCCGTC n876242
 1 ATGTCGCGA-----TCCAAACGGCGC g598956

41 AGCATGCCACACGGCTTCAGCCCCGGGACTTTGGTGTTCG n876242
 20 AGAACGA-GTAC-----AAATGCGGGGACCTGGTGTTCG g598956

81 CTAAGATGAAGGGCTACCCCTCACCTGGCCCTGGCCAGGATCGA n876242
 53 CCAAAGATGAAGGGCTACCCACACTGGCCCGGCCTGGAT[T]GA g598956

121 CGACATCGGGGATGGCGCCGTGAAAGCCCCAACAAAG n876242
 93 CAGCAT[GCGCTGAGCTGGCTACCCACAAAC[A]GCGCAACAAAG g598956

161 TACCCCCATCTTTCTTGGCACACACAGAAACAGCCTTCC n876242
 133 TACCAA[G]TCTTT[T]T[G]G[G]AC[CA]GG[G]AC[G]CAT[T]CC g598956

201 TGGCCCCAACAGACCTCTCCCTACAGGAAATCCAAGGA n876242
 173 TGGCCCCAACAGACCTCTCCCTACAGGAAATCCAAGGA g598956

241 GAAGTTGGCAAGCCCACAGGAAAGGGTTCAAGCGAG n876242
 213 GAAGTTGGCAAGCCCACAGGAAAGGGTTCAAGCGAG g598956

281 GGGCTGGAGAGATGGAGAACACCTACTGTCAAGGCTT n876242
 253 GGCTGGAGATGGAGAACACCTACTGTCAAGGCTT g598956

321 CCGGCTATCAGTCCCTCCAGAAAAAGAGCTGTGGAAAGA n876242
 293 CGGCTATCAGTCCCTCCAGAAAAAGAGCTGTGGAAAGA g598956

FIGURE 3A

TGTTGGGTGAGGAGGAGG

361 GCCTGAACCGAGCCCCGAAAGCTGCAGAGGGTACGGTGAT n876242
333 GCCTGAACCGAGCCCCGAAAGCTGCAGAGGGTACGGTGAT g598956

401 AAGAAGGGAAATGCAGAGGGCAGCCAGGACGGAGGAAGGAA n876242
373 AAGAAGGGAAATGCAGAGGGCAGCCAGGACGGAGGAAGGAA g598956

441 AGCTGGTCATTGATGAGCCAGGGCAAGGAGAACGAGAA n876242
413 AGCTGGTCATTGATGAGCCAGGGCAAGGAGAACGAGAA g598956

481 AGGAGCGTTGAAAGAGGAGAGCACGGGACTTGTGGAGGAC n876242
453 AGGAGCGTTGAAAGAGGAGAGCACGGGACTTGTGGAGGAC g598956

521 TCTCCTAAACGTCCTAAAGGAGGCCAGAAACCCCTGAAAGGAG n876242
493 TCTCCTAAACGTCCTAAAGGAGGCCAGAAACCCCTGAAAGGAG g598956

561 AGGAGAAGGAGGCAGCCACCTTGGAGGGCTTGAGAGGCCCT n876242
533 AGGAGAAGGAGGCAGCCACCTTGGAGGGCTTGAGAGGCCCT g598956

601 TCCCTATGGAGGTGGAAAGAATAGCACCCCCCTCTGAGCCC n876242
573 TCCCTATGGAGGTGGAAAGAATAGCACCCCCCTCTGAGCCC g598956

641 GGCTCTGGCGGGCCCTCCCCNNNNNNNNNNNNNNNN n876242
613 GGCTCTGGCGGGCCCTCCCCAAGAGGAAGAGAGGG G g598956

FIGURE 3B

FDR200: SINGEDEL

681 NNNNNNNNAGGAAGGGTACCAAGGAAAGATGCTGAGGC n876242
693 A GG AT GAA AG GAGGAAAGGGCTACCAAGGAAAGATGCTGAGGC g598956

721 CCCAGGCATCAAGAGTCATGAGGAGCCCTGTAGCCACCAATG n876242
693 CCCAGGCATCAGAGATCAATGAGGCCCTGTAG g598956

761 TTTCAAAGGAGGCCACCCCTGTTCTGCTGCTGTGG n876242
723

801 GTGCTACTGGGAAACTGGCCATGGCTGCACACTGGGNA n876242
723 g598956

841 CCCCTTTCCANCNCAANCCTGNTNTCTT n876242
723 g598956

FIGURE 3C

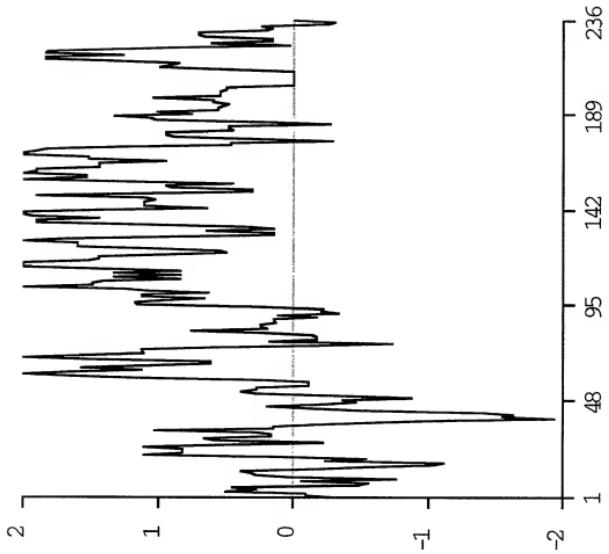


FIGURE 4A

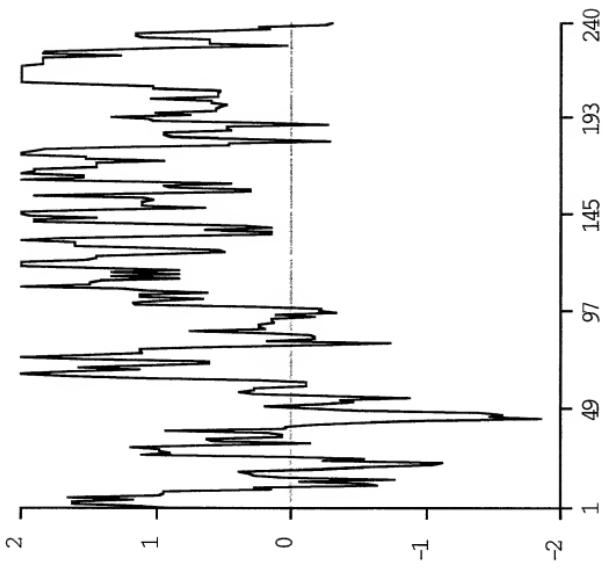


FIGURE 4B

Library	Lib Description	Abun	Pct Abun
HNT3AZT01	HNT2 cell line, teratocarcinoma, treated AZ	5	0.3425
THP1PLB02	THP-1 promonocyte cell line, treated PMA, LPS	4	0.1630
THP1PBE01	THP-1 promonocyte cell line, treated PMA	3	0.1463
PANCDIT03	pancreas, NIDDM, 57 M	1	0.1462
THP1T7T01	THP1 cells, untreated	3	0.1447
BSTMNTO01	brain stem, 72 M	1	0.1214
PROSTUT12	prostate tumor, 65 M, match to PROSN020	4	0.1118
HUVESTB01	HUVEC endothelial cell line, shear stress	3	0.1078
PENITUT01	penis tumor, carcinoma, 64 M	4	0.1066
AMLBNT01	AML blast cells, blast crisis, 58 F	1	0.1058
COLINNOT13	colon, ascending, 28 M	3	0.0932
HUVENOB01	HUVEC endothelial cell line, control	2	0.0841
UTRSNOT05	uterus, 45 F	3	0.0834
SINTNOT13	small intestine, ileum, ulcerative cholangitis, 25 F	3	0.0826
LUNGNOT03	lung tumor, 69 M, match to LUNGNOT15	5	0.0796
OVARNOM01	ovary, 49 F, WM	1	0.0752
PLACNOM02	placenta, neonatal F, NORM, WM	13	0.0722
PROSNOT01	prostate, 78 M	2	0.0702
SPLNFM01	spleen, fetal, WM	2	0.0663
COLINNOT19	large intestine, cecum, 18 F	2	0.0585
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	4	0.0580
COLNFET02	colon, fetal F	4	0.0571

FIGURE 5A

THP1NOT01	THP1 cells, untreated	1	0.0571
LUNGNTU02	lung tumor, metastasis, 79 M, match to LUNGNOT03	3	0.0567
SINTNOT01	small intestine, ileum, 4 F	2	0.0560
THP1AZT01	THP-1 promonocyte cell line, treated AZ	1	0.0554
LUNGNOT15	lung, 69 M, match to LUNGNTU03	2	0.0553
LIVRFET02	liver, fetal F	2	0.0550
KERANOT02	keratinocytes, primary cell line, 30 F	3	0.0546
PROSTUT09	prostate tumor, 66 M	2	0.0529
LEUKNOT03	white blood cells, 27 F	2	0.0523
TESTNT03	testis, 37 M	4	0.0515
COLNPOT01	colon polyp, 40 F	2	0.0513
PROSNOT14	prostate, 60 M, match to PROSTUT08	2	0.0512
BRAITUT02	brain tumor, metastasis, 58 M	3	0.0509
BRSTTU03	breast tumor, 58 F, match to BRSTNOT05	5	0.0493
TESTNOT01	testis, 37 M	1	0.0478
UCMCNOT02	mononuclear cells	2	0.0471
THP1PLB01	THP-1 promonocyte cell line, treated PMA, LPS	1	0.0452
BRSTNOT02	breast, 55 F, match to BRSTTU01	4	0.0443
PROSNOT02	prostate, 50 M, match to PROSTUT01	1	0.0435
COLNNOT08	colon, 60 M	1	0.0426
PANCNTU02	pancreatic tumor, carcinoma, 45 F	2	0.0403
SCORNOT01	spinal cord, 71 M	2	0.0402
UTRSNOT01	uterus, 59 F	1	0.0394
SINTTUT01	small intestine tumor, ileum, 42 M	1	0.0382

FIGURE 5B

FIGURE 5C: SISSES SECTION

TLYMMN01	lymphocytes (non-adher PBMC), 24 M, RP	1	0.0379
HNT2RAT01	HNT2 cell line, teratocarcinoma, treated RA	2	0.0376
BRAINOT03	brain, 26 M	2	0.0371
LUNGNOT04	lung, 2 M	2	0.0366
PROSNOT20	prostate, 65 M, match to PROSTUT12	1	0.0336
CARDFEM01	heart, fetal, NORM, WM	3	0.0335
OVARUTU01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0323
OVARNOT02	ovary, 59 F	1	0.0316
NEUTGM01	granulocytes, periph blood, M/F, treated GM-CSF	2	0.0313
BRSTNOT05	breast, 58 F, match to BRSTTU03	2	0.0309
STOMNOT02	stomach, 52 M, match to STOMTU01	1	0.0308
BRSTNOT07	breast, 43 F	1	0.0307
STOMNOT01	stomach, 55 M	1	0.0303
LUNGNOT18	lung, 66 F	1	0.0298
TONGTU01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITTU08	brain tumor, astrocytoma, 47 M	2	0.0293
COLINTU06	large intestine, cecal tumor, 45 F	1	0.0293
LIVSFEM02	liver/spleen, fetal M, NORM, WM	11	0.0290
BEPINOT01	bronchial epithelium, primary cell line, 54 M	2	0.0289
PANCNOT07	pancreas, fetal M	1	0.0287
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
LUNGNOT12	lung, 78 M	1	0.0278
TESTTU02	testicular tumor, 31 M	1	0.0278

FIGURE 5C

TUMOR TYPES IN THE TCGA

THYRTUT03	thyroid tumor, benign, 17 M	1	0.02776
LATRTUT02	heart tumor, myoma, 43 M	2	0.0275
BEPINON01	bronchial epithelium, 1° cell line, 54 M, NORM	1	0.0274
OVARNOT07	ovary, 28 F	1	0.0269
PTHYTOM01	parathyroid tumor, adenoma, M/F, NORM, WM	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
LATRNTO01	heart, left atrium, 51 F	1	0.0266
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266
BRSTNOM01	breast, F, NORM, WM	1	0.0264
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262
DUODNOT02	small intestine, duodenum, 8 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
BRAITUT07	brain tumor, left frontal, 32 M	1	0.0259
LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259
PROSNOT18	prostate, 58 M	1	0.0256
PANCNTO08	pancreas, 65 F, match to PANCTUT01	1	0.0254
BLADTUT04	bladder tumor, 60 M, match to BLADNOT05	2	0.0253
PLACMNB01	placenta, neonatal F	1	0.0251
LUNGNOT02	lung, 47 M	1	0.0246
TMLR3DT02	lymphocytes (non-adher PBMMC), M/F, 72-hr MLR	1	0.0246
HIPONOT01	brain, hippocampus, 72 F	1	0.0239
RATRNOT02	heart, right atrium, 39 M	1	0.0237
MMLRIDT01	macrophages (adher PBMMC), M/F, 24-hr MLR	1	0.0236

FIGURE 5D

TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	1	0.0229
PROSNTO06	prostate, 57 M, match to PROSTUT04	2	0.0228
LIVRNOT01	liver, 49 M	1	0.0198
COLNTUT03	colon tumor, 62 M, match to COLNNNOT16	1	0.0196
CRBLNOT01	brain, cerebellum, 69 M	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0194
BRSTNOT04	breast, 62 F	2	0.0192
MELANOM01	melanocytes, M, NORM, WM	2	0.0192
LUNGAST01	lung, asthma, 17 M	2	0.0189
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMNC), M/F, 48-hr MLR	1	0.0178
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174
HNT2NOT01	HNT2 cell line, teratocarcinoma, control	1	0.0173
UCMCL5T01	mononuclear cells, treated IL-5	2	0.0168
CONNNOT01	fat, mesentery, 71 M	1	0.0149
BRSTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	1	0.0134
SINTFET03	small intestine, fetal F	1	0.0130
KIDNNNOT05	kidney, neonatal F	1	0.0106
CORPNNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0103
BRSTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0095
LUNGFFET03	lung, fetal F	1	0.0091
BRANOM01	brain, infant F, NORM, WM	1	0.0045

FIGURE 5E